

SEQUENCE LISTING

<110> DAICEL CHEMICAL INDUSTRIES, LTD.

<120> NOVEL ENONE REDUCTASES, METHODS FOR PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A CARBON-CARBON DOUBLE BOND OF AN α, β -UNSATURATED KETONE USING THE REDUCTASES

<130> D1-A0103

<140>

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<150> JP 2001-049363

<151> 2001-02-23

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1113

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1).. (1113)

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Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr

Ins
A2

20	25	30	
gcc ttg gtg aag gtt gag gct gtt gct ggt aac cca act gat tgg aag			144
Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys			
35	40	45	
cat att gct tat aag att ggt cca gaa ggt tca att cta gga tgt gac			192
His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp			
50	55	60	
att gct ggt aca gtt gtc aaa ctt gga cca aat gct agt act gac ttg			240
Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu			
65	70	75	80
aag gtt gga gat acc ggt ttc ggt ttt gtt cac ggt gct tcc caa aca			288
Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr			
85	90	95	
gat cct aaa aat ggt gca ttt gct gaa tat gcc agg gtt tat cca cct			336
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro			
100	105	110	
ttg ttt tac aag agt aac tta act cac tca act gct gat gaa att tct			384
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser			
115	120	125	
gaa ggc cct gtg aag aac ttc gaa tct gct gca tca ttg cca gtt tcg			432
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser			
130	135	140	
ttg aca act gct ggt gtt agt ttg tgt cat cac ttg ggc tca aaa atg			480
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met			
145	150	155	160
gaa tgg cac cca tct acc ccg caa cat act cat cca tta ttg att tgg			528
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp			

165 170 175
 ggt ggt gct aca gca gtg ggt caa caa cta atc caa gtt gcc aaa cat 576
 Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His
 180 185 190
 atc aat gct tat act aag att gta act gtt gct tct aaa aag cat gaa 624
 Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu
 195 200 205
 aag ctt tta aag tct tat ggt gct gat gat gtc ttt gac tat cat gat 672
 Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp
 210 215 220
 gca ggc gtt att gag cag atc aaa tcg aag tat cca aac ctg caa cat 720
 Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His
 225 230 235 240
 gtt att gac gct gtg gga agc gaa gat agt atc ccc gag gcc tat aaa 768
 Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys
 245 250 255
 gtc aca gca gat agt cta cct gcc aca tta tta gaa gtg gtt cca atg 816
 Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met
 260 265 270
 acc att gaa agc att cct gaa gaa atc aga aaa gat aat gtt aaa att 864
 Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile
 275 280 285
 gat att act ttg ttg tat cgt gca tct ggt caa gaa att cta ttg ggt 912
 Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly
 290 295 300
 gca aca aga ttt cct gct agt cca gaa tat cat gaa gcc aca gtt aaa 960
 Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys

305 310 315 320
 ttc gtt aag ttt ata aat cca cac ctt aac aac ggt gat atc cat cat 1008
 Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His
 325 330 335
 atg aat att aaa gtt ttc agc aac ggc tta gat gat gtc cca gct ctc 1056
 Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu
 340 345 350
 act gaa ggt ata aaa gaa ggt aaa aac aaa aat gtt aag tat gtt gcc 1104
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 agg tta taa 1113
 Arg Leu
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 <213> Kluyveromyces lactis

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 Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys
 35 40 45
 His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp
 50 55 60
 Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu
 65 70 75 80
 Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr

	85	90	95
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro			
100	105	110	
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser			
115	120	125	
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser			
130	135	140	
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met			
145	150	155	160
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp			
165	170	175	
Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His			
180	185	190	
Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu			
195	200	205	
Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp			
210	215	220	
Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His			
225	230	235	240
Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys			
245	250	255	
Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met			
260	265	270	
Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile			
275	280	285	
Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly			
290	295	300	
Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys			
305	310	315	320
Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His			
325	330	335	
Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu			
340	345	350	
Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala			
355	360	365	
Arg Leu			

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<210> 3

<211> 1145

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (6).. (1136)

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aat ggc aag gct gta gtc aaa cag gac att cca att cct gaa tta gaa 98

Asn Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu

20

25

30

gaa gga ttt gtt cta att aag act gtc gcc gtt gcc ggt aac cct acc 146

Glu Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr

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40

45

gat tgg aaa cat att gat ttc aag att ggt cct caa ggt gcc ctc tta 194

Asp Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu

50

55

60

ggc tgt gat gca gcc ggc caa atc gta aag ttg ggc cca aat gtt gat 242

Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp

65

70

75

gct gca cgc ttt gcc att ggt gat tac att tat ggg gtt att cac ggt 290

Ala Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly

80	85	90	95
gct tca gtg agg ttc ccc tca aac ggt gcc ttt gct gag tac tct gcc 338			
Ala Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala			
100	105	110	
att tca tcc gag act gct tat aaa cca gcc aga gag ttt aga ttg tgc 386			
Ile Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys			
115	120	125	
ggt aaa gac aag cta cca gaa ggc ccc gta aaa tct tta gaa ggg gca 434			
Gly Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala			
130	135	140	
gta tcc ctc cca gtc tca ttg acc acg gct ggt atg atc ctt aca cat 482			
Val Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His			
145	150	155	
agt ttt ggc ttg gac atg aca tgg aag ccc tcc aaa gcg caa aga gat 530			
Ser Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp			
160	165	170	175
caa ccc atc tta ttt tgg ggt ggt gcc act gct gtt ggc cag atg ctt 578			
Gln Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu			
180	185	190	
att caa ttg gca aaa aaa cta aac ggt ttc agc aag atc atc gtc gtt 626			
Ile Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val			
195	200	205	
gct tct cgt aaa cat gaa aaa ttg ttg aaa gag tac ggt gca gat gaa 674			
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu			
210	215	220	
ctt ttt gac tac cac gat gct gac gtt atc gaa cag ata aaa aag aag 722			
Leu Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys			

225	230	235	
tac aac aac att cct tac ttg gtg gac tgt gtc tcc aac aca gaa act			770
Tyr Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr			
240	245	250	255
att caa cag gtg tac aaa tgt gcc gct gat gac tta gac gct acg gtc			818
Ile Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val			
260	265	270	
gtt caa ttg acc gtt tta acc gaa aaa gat atc aag gag gaa gac agg			866
Val Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg			
275	280	285	
agg caa aac gtc agt att gaa gga acc ctt cta tat ttg ata gga ggt			914
Arg Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly			
290	295	300	
aac gac gtc cca ttt ggc acg ttt act ttg cca gca gac cct gaa tac			962
Asn Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr			
305	310	315	
aag gaa gcc gcc ata aaa ttt att aag ttc atc aat cca aaa atc aat			1010
Lys Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn			
320	325	330	335
gat ggt gaa atc cac cac atc cca gtg aaa gtt tac aag aac ggg tta			1058
Asp Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu			
340	345	350	
gat gat atc cca cag tta ctt gat gat att aag cac ggg agg aat tct			1106
Asp Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser			
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<211> 376

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 4

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 20 25 30
 Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr Asp
 35 40 45
 Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu Gly
 50 55 60
 Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp Ala
 65 70 75 80
 Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly Ala
 85 90 95
 Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile
 100 105 110
 Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys Gly
 115 120 125
 Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala Val
 130 135 140
 Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His Ser
 145 150 155 160
 Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp Gln
 165 170 175
 Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu Ile
 180 185 190
 Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val Ala
 195 200 205
 Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu Leu

210	215	220
Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys Tyr		
225	230	235
Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr Ile		240
	245	250
Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val Val		255
	260	265
Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg Arg		270
	275	280
Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly Asn		285
	290	295
Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr Lys		300
305	310	315
Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn Asp		320
	325	330
Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu Asp		335
	340	345
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<222> (1).. (1134)

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1 5 10 15

gac ggt aaa gcg gtt gtt aaa gag ggc att ccc att cct gaa ttg gaa 96
Asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu
20 25 30

gaa gga ttc gta ttg att aag aca ctc gct gtt gct ggt aac ccc act 144
Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr
35 40 45

gat tgg gca cac att gac tac aag atc ggg cct caa gga tct att ctg 192
Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu
50 55 60

gga tgt gat gct gct ggc caa att gtc aaa ttg ggc cca gct gtc aat 240
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn
65 70 75 80

cct aaa gac ttt tct atc ggt gat tat att tat ggg ttc att cac gga 288
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly
85 90 95

tct tcc gta agg ttt cct tcc aat ggt gct ttt gct gaa tat tct gct 336
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
100 105 110

att tca act gtg gtt gcc tac aaa tca ccc aat gaa ctc aaa ttt ttg 384
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu
115 120 125

ggt gag gat gtt cta cct gcc ggc cct gtc agg tct ttg gaa ggt gta 432
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val
130 135 140

gcc act atc cca gtg tca ctg acc aca gcc ggc ttg gtg ttg acc tat 480
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr

12/27

145 150 155 160

aac ttg ggc ttg gac ctg aag tgg gag cca tca acc cca caa aga aaa 528
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys
165 170 175

ggc ccc atc tta tta tgg ggc ggt gca act gca gta ggt cag tcg ctc 576
Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu
180 185 190

atc caa tta gcc aat aaa ttg aat ggc ttc acc aag atc att gtt gtg 624
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val
195 200 205

gct tct cgg aag cac gaa aaa ctt ttg aaa gaa tat ggt gct gat gaa 672
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
210 215 220

tta ttt gat tat cat gat att gac gtg gta gaa caa att aaa cac aag 720
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys
225 230 235 240

tac aac aat atc tcg tat tta gtc gac tgt gtc gcg aat caa gat acg 768
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr
245 250 255

ctt caa caa gtg tac aaa tgt gcg gcc gat aaa cag gat gct aca att 816
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile
260 265 270

gtt gaa tta aaa aat ttg aca gaa gaa aac gtc aaa aaa gag aac agg 864
Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg
275 280 285

aga caa aac gtt act att gac ata ata agg cta tat tca ata ggt ggc 912
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly

290

295

300

cat gaa gta cca ttt gga aac att act tta cca gcc gac tca gaa gct 960

His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala

305

310

315

320

agg aaa gct gca ata aaa ttt atc aaa ttc atc aat cca aag att aat 1008

Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn

325

330

335

gat gga caa att cgc cat att cca gta agg gtc tat aag aac ggg ctt 1056

Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu

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345

350

tgt gat gtt cct cat atc cta aaa gac atc aaa tat ggt aag aac tct 1104

Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser

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360

365

ggg gaa aaa ctc gtt gcc gta tta aac taa

1134

Gly Glu Lys Leu Val Ala Val Leu Asn

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375

<210> 6

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<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 6

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Asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu

20

25

30

Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr

35

40

45

Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu

50 55 60
 Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn
 65 70 75 80
 Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly
 85 90 95
 Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala
 100 105 110
 Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu
 115 120 125
 Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val
 130 135 140
 Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr
 145 150 155 160
 Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys
 165 170 175
 Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu
 180 185 190
 Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val
 195 200 205
 Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu
 210 215 220
 Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys
 225 230 235 240
 Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr
 245 250 255
 Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile
 260 265 270
 Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg
 275 280 285
 Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly
 290 295 300
 His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala
 305 310 315 320
 Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
 325 330 335
 Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu

	340		345		350										
Cys	Asp	Val	Pro	His	Ile	Leu	Lys	Asp	Ile	Lys	Tyr	Gly	Lys	Asn	Ser
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Gly	Glu	Lys	Leu	Val	Ala	Val	Leu	Asn							
	370		375												

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<211> 1122

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (7).. (1113)

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Met Lys Ala Val Val Ile Glu Asp Gly Lys Ala Val Val Lys

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gag ggc gtt ccc att cct gaa ttg gaa gaa gga ttc gta ttg att aag 96

Glu Gly Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys

15

20

25

30

aca ctc gct gtt gct ggt aac ccg act gat tgg gca cac att gac tac 144

Thr Leu Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr

35

40

45

aag gtc ggg cct caa gga tct att ctg gga tgt gac gct gcc ggc caa 192

Lys Val Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln

50

55

60

att gtc aaa ttg ggc cca gcc gtc gat cct aaa gac ttt tct att ggt 240

Ile Val Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly

65	70	75	
gat tat att tat ggg ttc att cac gga tct tcc gta agg ttt cct tcc			288
Asp Tyr Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser			
80	85	90	
aat ggt gct ttt gct gaa tat tct gct att tca act gtg gtt gcc tac			336
Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr			
95	100	105	110
aaa tca ccc aat gaa ctc aaa ttt ttg ggt gaa gat gtt cta cct gcc			384
Lys Ser Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala			
115	120	125	
ggc cct gtc agg tct ttg gaa ggg gca gcc act atc cca gtg tca ctg			432
Gly Pro Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu			
130	135	140	
acc aca gct ggc ttg gtg ttg acc tat aac ttg ggc ttg aac ctg aag			480
Thr Thr Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys			
145	150	155	
tgg gag cca tca acc cca caa aga aac ggc ccc atc tta tta tgg ggc			528
Trp Glu Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly			
160	165	170	
ggt gca act gca gta ggt cag tcg ctc atc caa tta gcc aat aaa ttg			576
Gly Ala Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu			
175	180	185	190
aat ggc ttc acc aag atc att gtt gtg gct tct cgg aaa cac gaa aaa			624
Asn Gly Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys			
195	200	205	
ctg ttg aaa gaa tat ggt gct gat caa cta ttt gat tac cat gat att			672
Leu Leu Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile			

210

215

220

gac gtg gta gaa caa att aaa cac aag tac aac aat atc tcg tat tta 720
 Asp Val Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu
 225 230 235

gtc gac tgt gtc gcg aat caa aat acg ctt caa caa gtg tac aaa tgt 768
 Val Asp Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys
 240 245 250

gcg gcc gat aaa cag gat gct acc gtt gtc gaa tta act aat ttg aca 816
 Ala Ala Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr
 255 260 265 270

gaa gaa aac gtc aaa aag gag aat agg agg caa aat gtc act att gac 864
 Glu Glu Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp
 275 280 285

aga aca aga ctg tat tca ata ggc ggc cat gaa gta cca ttt ggt ggc 912
 Arg Thr Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly
 290 295 300

att act ttc cct gct gac cca gaa gcc agg aga gct gcc acc gaa ttc 960
 Ile Thr Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe
 305 310 315

gtc aag ttc atc aat cca aag att agt gat ggg caa att cac cat att 1008
 Val Lys Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile
 320 325 330

cca gca agg gtc tat aag aac ggg ctt tac gat gtt cct cgt atc ctg 1056
 Pro Ala Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu
 335 340 345 350

gaa gac att aaa atc ggt aag aac tct ggt gaa aaa ctc gtt gcc gta 1104
 Glu Asp Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val

355

360

365

1122

tta aac taa tctagaaac

Leu Asn

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<211> 368

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Lys Ala Val Val Ile Glu Asp Gly Lys Ala Val Val Lys Glu Gly
1 5 10 15
Val Pro Ile Pro Glu Leu Glu Gly Phe Val Leu Ile Lys Thr Leu
20 25 30
Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr Lys Val
35 40 45
Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln Ile Val
50 55 60
Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly Asp Tyr
65 70 75 80
Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser Asn Gly
85 90 95
Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr Lys Ser
100 105 110
Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala Gly Pro
115 120 125
Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu Thr Thr
130 135 140
Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys Trp Glu
145 150 155 160
Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly Gly Ala
165 170 175
Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu Asn Gly
180 185 190

Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys Leu Leu
 195 200 205
 Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile Asp Val
 210 215 220
 Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu Val Asp
 225 230 235 240
 Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys Ala Ala
 245 250 255
 Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr Glu Glu
 260 265 270
 Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp Arg Thr
 275 280 285
 Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly Ile Thr
 290 295 300
 Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe Val Lys
 305 310 315 320
 Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile Pro Ala
 325 330 335
 Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu Glu Asp
 340 345 350
 Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val Leu Asn
 355 360 365

<210> 9

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<212> PRT

<213> Kluyveromyces lactis

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Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp

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5

10

<210> 10

<211> 12

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<213> Kluyveromyces lactis

<400> 10

Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp Ile

1

5

10

<210> 11

<211> 20

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<221> misc_feature

<222> (12)

<223> n indicates g, a, c or t.

<400> 11

tgrtartcra anacrtcttc

20

<210> 12

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<222> (18)

<223> n indicates g, a, c or t.

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20

<210> 13

<211> 20

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tcccaaacag atcctaataaa tgggtgcattt gctgaaatag ccagggttta tccacctttg 180

tttacaaga gtaacttaac tcactcaact gctgatgaaa tttctgaagg ccctgtgaag 240
 aacttcgaat ctgctgcac attgccagtt tcgttgacaa ctgctgggtg tagtttgtgt 300
 catcacttgg gtcacaaaat ggaatggcac ccatctaccc cgcaacatac tcatccatta 360
 ttgatttggg gtgggtgctac agcagtgggt caacaactaa tccaagttgc caaacatata 420
 aatgcttata ctaagattgt aactgttgct tctaaaaagc atgaaaagct tttaaagtct 480
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<210> 15

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<212> DNA

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<210> 16

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<210> 17

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<210> 21

<211> 39

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<210> 22

<211> 25

<212> DNA

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<400> 22

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<210> 23

<211> 31

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<210> 28

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<212> DNA

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<223> Description of Artificial Sequence:an artificially synthesized primer sequence

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18

<210> 29

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 29

caggaaacag ctatgacc

18

Ins
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